

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 04:47:34 ; Search time 116.57 Seconds

(without alignments)
534,256 Million cell updates/sec

Title: US-09-719-748-2

Perfect score: 1846
Sequence: 1 MEPRKQKVEDFDYDGEELG.....TEEDTARKKALHPRRSSTS 360

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 segs, 17299429 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEA:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1835	99.4	370	4	075892
2	1824	98.8	370	4	09UIK4
3	1764	95.6	370	11	09QYK4
4	1481	80.2	303	11	088861
5	1297	70.3	1430	11	09JJP7
6	1293	70.0	367	4	09BTL8
7	1251.5	67.8	345	11	09CIV4
8	1166	63.2	454	4	043293
9	1140	61.8	448	11	054784
10	1140	61.8	448	11	088764
11	787	42.6	1435	5	044997
12	698	37.8	992	4	09C0L5
13	695	37.6	641	6	09B6E9
14	688.5	37.3	907	13	098850
15	668.5	36.2	611	11	091X59
16	663.5	36.1	2762	5	P91255

17	660	35.8	1721	5	0961U1	0961U1 drosophila
18	660	35.8	7107	5	09VAE7	09VAE7 drosophila
19	651.5	35.3	371	11	091X58	091X58 rattus norv
20	650	35.2	6658	5	076281	076281 drosophila
21	649.5	35.2	372	11	0923E7	0923E7 mus musculu
22	641	34.7	795	4	0960V1	0960V1 homo sapien
23	621.5	33.7	451	5	016980	016980 aplysia cal
24	603.5	32.7	596	4	09H1R3	09H1R3 homo sapien
25	594	32.2	577	5	09GV81	09GV81 drosophila
26	592	32.1	929	5	001651	001651 drosophila
27	591	32.0	732	5	09GVY1	09GVY1 drosophila
28	591	32.0	786	5	09GVY9	09GVY9 drosophila
29	591	32.0	832	5	001653	001653 drosophila
30	591	32.0	913	5	09V7G6	09V7G6 drosophila
31	589	31.9	1211	5	023260	023260 caenorhabd
32	586	31.7	569	5	001652	001652 drosophila
33	584.5	31.7	6831	5	023550	023550 caenorhabd
34	584.5	31.7	7160	5	023551	023551 caenorhabd
35	581	31.5	1289	4	09Y2A5	09Y2A5 homo sapien
36	580	31.4	2959	11	09JIF1	09JIF1 rattus norv
37	578.5	31.3	446	5	095SK9	095SK9 drosophila
38	571.5	31.0	335	5	061269	061269 mytilus gal
39	571.5	31.0	878	5	09GV22	09GV22 mytilus gal
40	564	30.6	357	4	09HD31	09HD31 homo sapien
41	553.5	30.6	623	5	09GV80	09GV80 drosophila
42	547	29.6	343	4	09NNY2	09NNY2 homo sapien
43	545	29.5	343	11	070150	070150 rattus norv
44	544.5	29.5	343	11	09GYK9	09GYK9 mus musculu
45	544	29.5	342	11	008767	008767 rattus norv

ALIGNMENTS

RESULT 1
ID 075892 PRELIMINARY; PRT; 370 AA.
AC 075892;
DT 01-NOV-1998 (TREMURel. 08, Created)
DT 01-NOV-1998 (TREMURel. 08, Last sequence update)
DT 01-DEC-2001 (TREMURel. 19, Last annotation update)
DE DAP-KINASE RELATED PROTEIN 1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=20094983; PubMed=10629061;
RA Inbal B., Shani G., Cohen O., Kissi J.L., Kimchi A.;
RT "Death-associated protein kinase-related protein 1, a novel
RT Serine/threonine kinase involved in apoptosis.";
RL Mol. Cell. Biol. 20:1044-1054(2000).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF052941; AAC35001.1;
DR HSSP: Q63450; 1A06
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 370 AA; 42923 MW; 0950284ADCD20P91 CRC64;

Query Match 99.4%; Score 1835; DB 4; Length 370;
Best Local Similarity 99.7%; Pred. No. 3, 2e-125;
Matches 359; Conservative 0; Mismatch 1; Indels 0; Gaps 0;
1 MEPRKQKVEDFDYDGEELGSGFATVKKCRKSTGLTAIRIKRQSRASRGVSRRE 60

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Db 11 MEPPFOQKVEDYDGEELGSGQFAIVKCKREKSTGLETAFAFKKRSRASRGVSREE 70
Qy 61 IEREVSILROVLHNNVITLHDYENRTDVAHLELVSGGELDFLAOKSISEEATSFTI 120
Db 71 IEREVSILROVLHNNVITLHDYENRTDVAHLELVSGGELDFLAOKSISEEATSFTI 130
Qy 121 KOILDGVNVLHRTKKAHFDLKPENIMLDKNIPPIHKLIDFGLAHEIDGVEFNKIGCT 180
Db 121 KOILDGVNVLHRTKKAHFDLKPENIMLDKNIPPIHKLIDFGLAHEIDGVEFNKIGCT 190
Qy 191 PEFVAPEIYNVEPLGLEADMSIGVITYTLLSGASPLDGTQOETLANITVSYPDEEF 240
Db 191 PEFVAPEIYNVEPLGLEADMSIGVITYTLLSGASPLDGTQOETLANITVSYPDEEF 250
Qy 241 FSHTESEAKDFTRKLLVETKRLTIQOELRHPWITPVNOQAMVRESVNLNFRKQY 300
Db 251 FSHTESEAKDFTRKLLVETKRLTIQOELRHPWITPVNOQAMVRESVNLNFRKQY 310
Qy 301 VRRRKLSFSIYSLCNHLTRSLMKKVHLRPDDDLNRCESDTEEDTARRKALHPRRRSSTS 360
Db 311 VRRRKLSFSIYSLCNHLTRSLMKKVHLRPDDDLNRCESDTEEDTARRKALHPRRRSSTS 370

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RESULT 2
Q9UIK4 PRELIMINARY: PRT: 370 AA.
ID 09UIK4
AC 09UIK4
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE DEATH-ASSOCIATED PROTEIN KINASE 2.
GN DAPK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99303018; PubMed=10376525;
RA Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Akira S.;
RT "Death-associated protein kinase 2 is a new calcium/calmodulin-
RT dependent protein kinase that signals apoptosis through its catalytic
RT activity."
RL Oncogene 18:3471-3480(1999).
CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB018001; BAA88063.1;
DR HSSP: Q63450; 1A06.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKC.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 370 AA: 42898 MW: 035E914BBD881A2 CRC64;

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Query Match 98.8%; Score 1824; DB 4; Length 370;
Best Local Similarity 99.2%; Pred. No. 2e-124;
Matches 357; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MEPPFOQKVEDYDGEELGSGQFAIVKCKREKSTGLETAFAFKKRSRASRGVSREE 60
Db 11 MEPPFOQKVEDYDGEELGSGQFAIVKCKREKSTGLETAFAFKKRSRASRGVSREE 70
Qy 61 IEREVSILROVLHNNVITLHDYENRTDVAHLELVSGGELDFLAOKSISEEATSFTI 120
Db 71 IEREVSILROVLHNNVITLHDYENRTDVAHLELVSGGELDFLAOKSISEEATSFTI 130

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Qy 121 KOILDGVNVLHRTKKAHFDLKPENIMLDKNIPPIHKLIDFGLAHEIDGVEFNKIGCT 180
Db 121 KOILDGVNVLHRTKKAHFDLKPENIMLDKNIPPIHKLIDFGLAHEIDGVEFNKIGCT 190
Qy 181 PEFVAPEIYNVEPLGLEADMSIGVITYTLLSGASPLDGTQOETLANITVSYPDEEF 240
Db 181 PEFVAPEIYNVEPLGLEADMSIGVITYTLLSGASPLDGTQOETLANITVSYPDEEF 250
Qy 241 FSHTESEAKDFTRKLLVETKRLTIQOELRHPWITPVNOQAMVRESVNLNFRKQY 300
Db 251 FSHTESEAKDFTRKLLVETKRLTIQOELRHPWITPVNOQAMVRESVNLNFRKQY 310
Qy 301 VRRRKLSFSIYSLCNHLTRSLMKKVHLRPDDDLNRCESDTEEDTARRKALHPRRRSSTS 360
Db 311 VRRRKLSFSIYSLCNHLTRSLMKKVHLRPDDDLNRCESDTEEDTARRKALHPRRRSSTS 370

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RESULT 3
Q9OYM4 PRELIMINARY: PRT: 370 AA.
ID 09OYM4
AC 09OYM4
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE DEATH-ASSOCIATED PROTEIN KINASE 2.
GN DAPK2 OR DAPK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99303018; PubMed=10376525;
RA Kawai T., Nomura F., Hoshino K., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Akira S.;
RT "Death-associated protein kinase 2 is a new calcium/calmodulin-
RT dependent protein kinase that signals apoptosis through its catalytic
RT activity."
RL Oncogene 18:3471-3480(1999).
CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB018002; BAA88064.1;
DR HSSP: Q63450; 1A06.
DR MGD: MGI:1341297; DapK2.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKC.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 370 AA: 42769 MW: 7DA6E29C4E6615B3 CRC64;

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Query Match 95.6%; Score 1764; DB 11; Length 370;
Best Local Similarity 96.4%; Pred. No. 4.4e-120;
Matches 347; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MEPPFOQKVEDYDGEELGSGQFAIVKCKREKSTGLETAFAFKKRSRASRGVSREE 60
Db 11 MEPPFOQKVEDYDGEELGSGQFAIVKCKREKSTGLETAFAFKKRSRASRGVSREE 70
Qy 61 IEREVSILROVLHNNVITLHDYENRTDVAHLELVSGGELDFLAOKSISEEATSFTI 120
Db 71 IEREVSILROVLHNNVITLHDYENRTDVAHLELVSGGELDFLAOKSISEEATSFTI 130
Qy 121 KOILDGVNVLHRTKKAHFDLKPENIMLDKNIPPIHKLIDFGLAHEIDGVEFNKIGCT 180
Db 121 KOILDGVNVLHRTKKAHFDLKPENIMLDKNIPPIHKLIDFGLAHEIDGVEFNKIGCT 190

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